```
RESULT 2
Q33C84_9APHY
ID   Q33C84_9APHY     PRELIMINARY;     PRT;    570 AA.
AC   Q33C84;
DT   06-DEC-2005, integrated into UniProtKB/TrEMBL.
DT   06-DEC-2005, sequence version 1.
DT   07-FEB-2006, entry version 3.
DE   Glucoamylase.
GN   Name=gla
OS   Fomitopsis palustris.
OC   Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC   Aphyllophorales; Fomitopsis.
OX   NCBI_TaxID=185425;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FFPRI 0507;
RA   Yoon J., Igarashi K., Kajisa T., Samejima M.;
RT   "Characterization and Molecular Cloning of Glycoside Hydrolase Family
RT   15 Glucoamylase from the brown-rot basidiomycete Fomitopsis
RT   palustris.";
RL   Submitted (OCT-2005) to the EMBL/GenBank/DDBJ databases.
CC   -----------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----------------------------------------------------------------------
DR   EMBL; AB239766; BAE47183.1; -; mRNA.
DR   GO; GO:0003824; F:catalytic activity; IEA.
DR   GO; GO:0004339; F:glucan 1,4-alpha-glucosidase activity; IEA.
DR   GO; GO:0005976; P:polysaccharide metabolism; IEA.
SQ   SEQUENCE 570 AA; 61247 MW; E77CE3BAC567702B CRC64;

Query Match             74.0%;  Score 1738.5;  DB 2;  Length 570;
Best Local Similarity   73.6%;  Pred. No. 1.8e-118;
Matches   332;  Conservative  46;  Mismatches  72;  Indels  1;  Gaps  1;

Qy    3 ASATAYLTKESAVAKNGVLCNIGSQGCMSEGAYSGIVIASPSKTSPDYLYTWTRDSSLVF 62
         ||:|||:||||| |||||| |||| ||  ||| :||||||||||:|::||||||||||:|
Db   19 SNVTSYISTETPLAKAGVLANIGPDGSLSSGAKSGIVIASPSTVNPDYLYTWTRDSSLTF 78

Qy   63 KQMLIDQYTNGLDTTLRTLIDEFVSARATIQQTSNPSGTVSTGGLGEPKFNIDETAPTGAW 122
         |: ||||:  |:||||  ||::|.|| ::|||: ||||:||||||||||:||| |.|| ||
Db   79 KALIDQFVSGEDDTLGPLIDDFTSAQAIIQQIDNPSGSVSTGGLGEPKFNIDEAFTGAW 138

Qy  123 GRPQRDGPALRATAIMTYATYLYNNGNTSVYTNTLWPIIKLDLDYVNSDWNQTTFDLWEE 182
         |||||||||||||||||||||||.||||: : :|||||  ||::||:   :  |||||||
Db  139 GRPQRDGPALRATAIMTYATYLYNSGNTTYVDTLWPIIELDLNYVATYWNESTFDLWEE 198

Qy  183 VDSSSFFTTAVQHRALVQGAAFATLIGQTSSASTYSATAPSILCFLQSYWN-TNGYWTAN 241
```

```
Qy  121 AWGRPQRDGPALRATAIMTYATYLYNNGNTSVYTNTLWPIIKLDLDYVNSDWNQTTFDLW 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  139 AWGRPQRDGPALRATAIMTYATYLYNNGNTSVYTNTLWPIIKLDLDYVNSDWNQTTFDLW 198

Qy  181 EEVDSSSFFTTAVQHRALVQGAAFATLIGQTSSASTYSATAPSILCFLQSYWNTNGWTA 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  199 EEVDSSSFFTTAVQHRALVQGAAFATLIGQTSSASTYSATAPSILCFLQSYWNTNGWTA 258

Qy  241 NTGGGRSGKDANTILASIHTFDASAGCSAATSQPCSDVALANLKVYVDSFRSIYTINSGI 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  259 NTGGGRSGKDANTILASIHTFDASAGCSAATSQPCSDVALANLKVYVDSFRSIYTINSGI 318

Qy  301 SSTSGVATGRYPEDSYYNGNPWYLCTLAVAEQLYDALIVWKAAGELNVTSVSLAFFQQFD 360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  319 SSTSGVATGRYPEDSYYNGNPWYLCTLAVAEQLYDALIVWKAAGELNVTSVSLAFFQQFD 378

Qy  361 SSITAGTYASSSVYTSLISDIQAFADEFVDIVAKYTPSSGFLSEQYDKSTGAQDSAANL 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  379 SSITAGTYASSSVYTSLISDIQAFADEFVDIVAKYTPSSGFLSEQYDKSTGAQDSAANL 438

Qy  421 TWSYAAAITAYQARNGFTGASWGAKGVSTSCST 453
         |||||||||||||||||||||||||||||||||
Db  439 TWSYAAAITAYQARNGFTGASWGAKGVSTSCST 471
```

```
Db  199 VDSSSFFTTAVQHRALREGITPANLIGETSDVSNWETQADDLLCFLQSYWNPTDLYMTAN 258
Qy  242 TGGGRSGKDANTILASIHTFDASAGCSAATSQPCSDVALANLKVYVDSFRSIYTINSGIS 301
Db  259 TGGGRSGKDANTVLASIHTFDPEAGCDDVTFQPCSDKALSNLKVYVDSFRSIYTINSGIS 318
Qy  302 STSGVATGRYPEDSYYNGNPWYLCTLAVAEQLYDALIVWKAAGELNVTSVSLAFFQQFDS 361
Db  319 SDAAVATGRYPEDSYYNGNPWFLTTLAAAEQLYDALIVWNAQGSLNVTSTSLAFFQQFDS 378
Qy  362 SITAGTYASSSVYTSLISDIQAFADEFVDIVAKYTPSSGFLSEQYDKSTGAQDSAANLT 421
Db  379 SVTAGTYASGSDEFTTLTSAIQTFADGFVEIIAKYTPSNGSLSEQYSKSDGSELSAYDLT 438
Qy  422 WSYAAAITAYQARNGFTGASWGAKGVSTSCS 452
Db  439 WSFAAALTAFEARAGNTYGSWGAANLTTSCS 469
```

```
RESULT 3
Q9P4C5_LENED
ID   Q9P4C5_LENED     PRELIMINARY;     PRT;    571 AA.
AC   Q9P4C5;
DT   01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2000, sequence version 1.
DT   07-FEB-2006, entry version 23.
DE   Glucoamylase.
OS   Lentinula edodes (Shiitake mushroom) (Lentinus edodes).
OC   Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC   Agaricales; Tricholomataceae; Lentinula.
OX   NCBI_TaxID=5353;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20292826; PubMed=10831434;
RX   DOI=10.1128/AEM.66.6.2531-2535.2000;
RA   Zhao J., Chen Y.H., Kwan H.S.;
RT   "Molecular cloning, characterization, and differential expression of a
RT   glucoamylase gene from the basidiomycetous fungus Lentinula edodes.";
RL   Appl. Environ. Microbiol. 66:2531-2535(2000).
CC   -----------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----------------------------------------------------------------------
DR   EMBL; AF220541; AAF75523.1; -; mRNA.
DR   HSSP; P04064; 1GAI.
DR   GO; GO:0003824; F:catalytic activity; IEA.
DR   GO; GO:0004339; F:glucan 1,4-alpha-glucosidase activity; IEA.
DR   GO; GO:0000272; P:polysaccharide catabolism; IEA.
DR   InterPro; IPR008291; Glucamylase_SBD.
DR   InterPro; IPR011613; Glyco_hydro15rel.
DR   InterPro; IPR000165; Glyco_hydro_15.
DR   InterPro; IPR002044; Glyco_hydro_s_bd.
DR   InterPro; IPR012343; Glyco_trans_sub.
DR   Pfam; PF00686; CBM_20; 1.
DR   Pfam; PF00723; Glyco_hydro_15; 1.
DR   PIRSF; PIRSF001031; Glu-a-glcsd_SBD; 1.
DR   PRINTS; PR00736; GLHYDRLASE15.
DR   ProDom; PD001568; Glyco_hydro_CBD; 1
SQ   SEQUENCE 571 AA; 61162 MW; A1BD1ECC848B97FF CRC64;

Query Match             66.4%;  Score 1560;  DB 2;  Length 571;
Best Local Similarity   64.7%;  Pred. No. 2.1e-105;
Matches   292;  Conservative  64;  Mismatches  95;  Indels  0;  Gaps  0;

Qy    1 QSASATAYLTKESAVAKNGVLCNIGSQGCMSEGAYSGIVIASPSKTSPDYLYTWTRDSS 60
         ||: :| ::|||:||| |::||:||| ||  ||| .|||||||||::|:||||||||||:|
Db   18 QSSVIDAYVASESPIAKASMLANIGPSGSKSSGAFSGIVIASPSTENPDYLYTWTRDSAL 77

Qy   61 VFKMLIDQYTNGLDTTLRTLIDEFVSARATIQQTSNPSGTVSTGGLGEPKFNIDETAFTG 120
         .::::||||:. |.|||||| :||::: |.|.:||: ||| :|||||||||||:||||||
Db   78 TFQTIIDQFTLGFDTTLRAEIDNYVGAQAIVQQIPNPSDITTGGLGEPKFYVNETAFTG 137
```

```
                    GenCore version 5.1.9
         Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:    October 30, 2006, 15:30:46 ; Search time 216.003 Seconds
                                         (without alignments)
                                2479.522 Million cell updates/sec

Title:     US-10-578-992-2
Perfect score:  3001
Sequence:  1 MFRSLLALAACAVASVSAQS.........REITTPASGTYTEKDTWDES 579

Scoring table:  BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:  2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters:   2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  UniProt_7.2:*
            1: uniprot_sprot:*
            2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2993[3]	99.7	579	2	Q12596_9APHY	athelia rol
2	2044	68.1	570	2	Q33C84_9APHY	fomitopsis
3	1849	61.6	571	2	Q9P4C5_LENED	lentinula e
4	1592	53.0	631	2	Q4WIT7_ASPFU	aspergillus
5	1576.5	52.5	639	1	AMYG_ASPSH	aspergillus
6	1576.5	52.5	639	2	Q76L57_ASPAW	aspergillus
7	1576	52.5	640	1	AMYG_ASPAW	aspergillus
8	1576	52.5	640	2	AMYG_ASPNG	aspergillus
9	1575	52.5	640	2	Q6DNI5_ASPNG	aspergillus
10	1565	52.1	640	2	Q6DUY5_ASPFI	aspergillus
11	1558.5	51.9	639	1	AMYG_ASPKA	aspergillus
12	1553.5	51.8	639	2	Q12537_ASPAW	aspergillus
13	1534.5	51.1	639	2	Q870G8_ASPNG	aspergillus
14	1530	51.0	612	2	Q3HLW7_ASPOR	aspergillus
15	1524	50.8	612	1	AMYG_ASPOR	aspergillus
16	1499.5	50.0	626	1	AMYG_NEUCR	neurospora
17	1473.5	49.1	618	2	Q9C1V4_TALEM	talaromyces
18	1463.5	48.8	661	2	Q5AWC8_EMENI	aspergillus
19	1411.5	47.0	617	2	Q5BHN1_THELA	thermomyces
20	1353	45.1	582	2	Q4HUN2_GIBZE	gibberella
21	1332.5	44.4	613	2	Q4WFY4_ASPFU	aspergillus
22	1330.5	44.3	620	2	Q12623_9ASCO	humicola gr
23	1310	43.7	616	1	AMYG_HORRE	hormoconis
24	1294.5	43.1	579	2	Q41930_GIBZE	gibberella
25	1204.5	40.1	1264	2	Q5AS26_EMENI	aspergillus
26	1200.5	40.0	493	2	Q2ULP9_ASPOR	aspergillus
27	1195	39.8	620	2	Q599K8_TRIHA	trichoderma
28	1194.5	39.8	493	2	O59846_ASPOR	aspergillus
29	1183	39.4	488	2	Q76KF7_PENCH	penicillium
30	897.5	29.9	547	2	Q4P749_USTMA	ustilago ma
31	779.5	26.0	609	2	Q8J0P8_MUCCI	mucor circi
32	765.5	25.5	604	2	Q2VC81_RHIOR	rhizopus or
33	747.5	24.9	604	2	AMYG_RHIOR	rhizopus or
34	746.5	24.9	579	2	Q7Z7X9_RHIOR	rhizopus or
35	715.5	23.8	480	2	Q2VER8_RHIOR	rhizopus or
36	696.5	23.2	450	2	AMYG_SCHPO	schizosacch
37	683.5	22.8	577	2	Q55SB7_CRYNE	cryptococcu
38	671.5	22.4	577	2	Q5KGR4_CRYNE	cryptococcu
39	633.5	21.1	624	2	AMYG_ARXAD	arxula aden
40	631	21.0	624	1	AMYH_SACFI	saccharomyc
41	626	20.9	519	1	Q6C6Y8_YARLI	yarrowia li
42	624	20.8	519	1	AMYG_SACFI	saccharomyc
43	615.5	20.5	515	2	Q8TPE5_SACFI	saccharomyc
44	565.5	18.8	564	2	Q5A773_CANAL	candida alb
45	538.5	17.9	545	2	Q6BYS6_DEBHA	debaryomyce

ALIGNMENTS

```
RESULT 1
Q12596_9APHY
ID   Q12596_9APHY    PRELIMINARY;  PRT;  579 AA.
AC   Q12596;
DT   01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT   01-NOV-1996, sequence version 1.
DT   07-FEB-2006, entry version 31.
DE   Glucoamylase G2 (EC 3.2.1.3).
OS   Athelia rolfsii.
OC   Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC   Aphyllophorales; Corticiaceae; Athelia.
OX   NCBI_TaxID=39291;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=AHU9627;
RX   MEDLINE=96158471; PubMed=8597548; DOI=10.1007/s002530050581;
RA   Nagasaka Y., Muraki N., Kimura A., Suto M., Yokota A., Tomita F.;
RT   "Cloning of Corticium rolfsi glucoamylase cDNA and its expression in
RT   Saccharomyces cerevisiae.";
RL   Appl. Microbiol. Biotechnol. 44:451-458(1995).
CC   -----------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----------------------------------------------------------------------
DR   EMBL; D49448; BAA08436.1; -; mRNA.
DR   HSSP; P04064; 1GAI.
DR   GO; GO:0004339; F:glucan 1,4-alpha-glucosidase activity; IEA.
DR   GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR   GO; GO:0000272; P:polysaccharide catabolism; IEA.
DR   InterPro; IPR008291; Glucamylase_SBD.
DR   InterPro; IPR011613; Glyco_hydro15rel.
DR   InterPro; IPR000165; Glyco_hydro_15.
DR   InterPro; IPR002044; Glyco_hydro_s_bd.
DR   InterPro; IPR012343; Glyco_trans_sub.
DR   Pfam; PF00686; CBM_20; 1.
DR   Pfam; PF00723; Glyco_hydro_15; 1.
DR   PIRSF; PIRSF001031; Glu-a-glcsd_SBD; 1.
DR   PRINTS; PR00736; GLHYDRLASE15.
DR   ProDom; PD001568; Glyco_hydro_CBD; 1.
KW   Glycosidase; Hydrolase.
SQ   SEQUENCE  579 AA;  61549 MW;  FF56D83F9D1A9EC9 CRC64;

Query Match        99.7%;    Score 2993;   DB 2;   Length 579;
Best Local Similarity  99.8%;   Pred. No. 1.2e-190;
Matches  578; . Conservative  0; Mismatches  0; Indels  1; Gaps  0;

Qy   1 MFRSLLALAACAVASVSAQSASATAYLTKESAVAKNGVLCNIGSQGCMSEGAYSGIVIAS 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MFRSLLALAACAVASVSAQSASATAYLTKESAVAKNGVLCNIGSQGCMSEGAYSGIVIAS 60

Qy  61 PSKTSPDYLYTWTRDSSLVFKMLIDQYTNGLDTTLRTLIDEFVSAEATIQQTSNPSGTVS 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61 PSKTSPDYLYTWTRDSSLVFKMLIDQYTNGLDTTLRTLIDEFVSAEATIQQTSNSSGTVS 120
```

RESULT 2

```
Qy  121 TGGLGEPKFNIDETAFTGAWGRPQRDGPALRATAIMTYATYLYNNGNTSYVTNTLWPIIK 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 TGGLGEPKFNIDETAFTGAWGRPQRDGPALRATAIMTYATYLYNNGNTSYVTNTLWPIIK 180

Qy  181 LDLDYVNSDWNQTTFDLWEEVDSSSFFTTAVQHRALVQGAAFATLIGQTSSASTYSATAP 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 LDLDYVNSDWNQTTFDLWEEVDSSSFFTTAVQHRALVQGAAFATLIGQTSSASTYSATAP 240

Qy  241 SILCFLQSYWNTNGYWTANTGGGRSGKDANTILASIHTFDASAGCSAATSQPCSDVALAN 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 SILCFLQSYWNTNGYWTANTGGGRSGKDANTILASIHTFDASAGCSAATSQPCSDVALAN 300

Qy  301 LKVYVDSFRSIYTINSGISSTSGVATGRYPEDSYYNGNPWYLCTLAVAEQLYDALIVWKA 360
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 LKVYVDSFRSIYTINSGISSTSGVATGRYPEDSYYNGNPWYLCTLAVAEQLYDALIVWKA 360

Qy  361 AGELNVTSVSLAFPQQFDSSITAGTYASSSSVVTSLISDIQAFADEFVDIVAKYTPSSGF 420
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 AGELNVTSVSLAFPQQFDSSITAGTYASSSSVVTSLISDIQAFADEFVDIVAKYTPSSGF 420

Qy  421 LSEQYDKSTGAQDSAANLTWSYAAAITAYQARNGFTGASWGAKGVSTSCSTGATSPGGSS 480
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 LSEQYDKSTGAQDSAANLTWSYAAAITAYQARNGFTGASWGAKGVSTSCSTGATSPGGSS 480

Qy  481 GSVEVTFDVYATTVYGQNIYITGDVSELGNWTPANGVALSSANYPTWSATIALPADTTIQ 540
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 GSVEVTFDVYATTVYGQNIYITGDVSELGNWTPANGVALSSANYPTWSATIALPADTTIQ 540

Qy  541 YKYVNIDGSTVIWEDAISNREITTPASGTYTEKDTWDES 579
        |||||||||||||||||||||||||||||||||||||||
Db  541 YKYVNIDGSTVIWEDAISNREITTPASGTYTEKDTWDES 579
```

```
RESULT 2
Q33CE4_9APHY
ID   Q33CE4_9APHY    PRELIMINARY;    PRT;    570 AA.
AC   Q33CE4;
DT   06-DEC-2005, integrated into UniProtKB/TrEMBL.
DT   06-DEC-2005, sequence version 1.
DT   07-FEB-2006, entry version 3.
DE   Glucoamylase.
GN   Name=gla;
OS   Pomitopsis palustris.
OC   Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC   Aphyllophorales; Fomitopsis.
OX   NCBI_TaxID=186125;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FFPRI 0507;
RA   Yoon J., Igarashi K., Kajisa T., Samejima M.;
RT   "Characterization and Molecular Cloning of Glycoside Hydrolase Family
RT   15 Glucoamylase from the brown-rot basidiomycete Fomitopsis
RT   palustris.";
RL   Submitted (OCT-2005) to the EMBL/GenBank/DDBJ databases.
```

```
DR   EMBL; AB239766; BAE47183.1; -; mRNA.
DR   GO; GO:0003824; F:catalytic activity; IEA.
DR   GO; GO:0004339; F:glucan 1,4-alpha-glucosidase activity; IEA.
DR   GO; GO:0005976; P:polysaccharide metabolism; IEA.
SQ   SEQUENCE   570 AA;  61247 MW;  E77CE3BAC56A702B CRC64;
```

```
Query Match             68.1%;  Score 2044;  DB 2;  Length 570;
Best Local Similarity   69.3%;  Pred. No. 1.8e-127;
Matches   399;  Conservative  63;  Mismatches  104;  Indels  10;  Gaps  5;

Qy    3 RSLLALAACAVASVSAQSASATAYLTKESAVAKNGVLCNIGSQGCMSEGAYSGIVIASPS 62
          |||  ||| |: :|||:: |:|:::|||  ||| | ||  |  |     |||||| ||
Db    2 RLSLSFVLGLVAAAFAQS-NVTSYISTETPLAKAGVLANIGPDGSLSSGAKSGIVIASPS 60

Qy   63 KTSPDYLYTWTRDSSLVFKMLIDQYTNGLDTTLRTLIDEFVSARATIQQTSNPSGTVSTG 122
```

RESULT 3

```
Qy   61 ...
        :|||||||||||| :|| :||||:|| ::|||| | |||| ::|| |||| |::|| | ||
Db   61 TVNPDYLYTWTRDSSLTFKALIDQFVSGEDDTLGPLIDDFTSAQAIIQQIDNPSGGVSVSTG 120

Qy  123 GLGEPKFNIDETAFTGAWGRPQRDGPALRATAIMTYATYLYNNGNTSYVTNTLWPIIKLD 182
        ||||||||||||||||||||||||||||||||||||||||||:||||:||:|||||:||
Db  121 GLGEPKFNIDETAFTGAWGRPQRDGPALRATAIMTYATYLYNSGNTTYVTDTLWPIIELD 180

Qy  183 LDYVNSDWNQTTFDLWEEVDSSSFFTTAVQHRALVQGAAFATLIGQTSSASTYSATAPSI 242
        |:| : :||::|||||||||||||||||||||||: ||  | :||| |  | |  ||::|
Db  181 LNTVATYWNESTFDLWEEVDSSSFFTTAVQHRALREGITFANLIGETSDVSNWETQADDL 240

Qy  243 LCFLQSYYNN-TNGWTANTGGGRSGKDANTILASIHTFDASAGCSAATSQPCSDVALANL 301
        ||||||| :|  | | ||||||||||||||:|||||||| :||  | |  ||||:||:||
Db  241 LCFLQSYVNPTDLYMTANTGGGRSGKDANTVLASIHTFDPEAGCDDVFQPCSDKALSNL 300

Qy  302 KVYVDSFRSIYTINSGISSTSGVATGRYPEDSYYNGNPWYLCTLAVAEQLYDALIVWKAA 361
        ||||||||||||||||||| : |||||||||||||||||:| ||||| |||||||||:|
Db  301 KVYVDSFRSIYTINSGISSDAAVATGRYPEDSYYNGNPWFLTTLAAAAEQLYDALIVWNAQ 360

Qy  362 GELNVTSVSLAFPQQFDSSITAGTYASSSSVYTSLISDIQAFADEFVDIVAKYTPSSGFL 421
        | |||||:||||||||||| :||||| ||:     |:||| ||| || :|||||||:| |
Db  361 GSLNVTSTSLAFPQQFDSSVTAGTYASGSDEFTTLTSAIQTFADGFVBIIAKYTPSNGSL 420

Qy  422 SEQYDKSTGAQDSAANLTWSYAAAITAYQARNGFTGASWGAKGVSTSCSTGATSPGGSSG 481
        ||| :|  |: ||:|::| | ::| || :|| |::|||||| |:::::| |     ||||
Db  421 SEQYSKSDGSELSAYDWTWSFAAALTAFEARAGNTYGSWGAANLTTSCS------GGSSG 474

Qy  482 S-VEVTFDVYATTVYGQNIYITGDVSELGNWTPANGVALSSANYPTWSATIALPADTTIQ 540
        | ||:||:| :::| |:|:||| ||||  |: : |: |:| ||:|||| | | ||:|||
Db  475 STVAVTFTVNYDVWGENLYITQSVSELSDWSTSSALIMSAADYPTWSITVDLPASTTIQ 534

Qy  541 YKYVNIDGSTVIWEDAISNREITTPASGTYTEKDTW 576
        |||: | ||:|:|||| :|::|||||||: |: |:|
Db  535 YKYITIYDGTVTWEDD-PNNEITTPASGSVTQADSW 569
```

```
RESULT 3
Q9P4C5_LENED
ID   Q9P4C5_LENED    PRELIMINARY;    PRT;    571 AA.
AC   Q9P4C5;
DT   01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2000, sequence version 1.
DT   07-FEB-2006, entry version 23.
DE   Glucoamylase.
OS   Lentinula edodes (Shiitake mushroom) (Lentinus edodes)
OC   Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC   Agaricales; Tricholomataceae; Lentinula.
OX   NCBI_TaxID=5353;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20292826; PubMed=10831434;
RX   DOI=10.1128/AEM.66.6.2531-2535.2000;
RA   Zhao J., Chen Y.H., Kwan H.S.;
RT   "Molecular cloning, characterization, and differential expression of a
RT   glucoamylase gene from the basidiomycetous fungus Lentinula edodes";
RL   Appl. Environ. Microbiol. 66:2531-2535(2000).
```

```
DR   EMBL; AF220541; AAF75523.1; -; mRNA.
DR   HSSP; P04064; 1GAI.
DR   GO; GO:0003824; F:catalytic activity; IEA.
DR   GO; GO:0004339; F:glucan 1,4-alpha-glucosidase activity; IEA.
DR   GO; GO:0000272; P:polysaccharide catabolism; IEA.
DR   InterPro; IPR008291; Glucamyl6e_SBD.
DR   InterPro; IPR011613; Glyco_hydro15rel.
DR   InterPro; IPR000165; Glyco_hydro_15.
DR   InterPro; IPR002044; Glyco_hydro_s_bd.
DR   InterPro; IPR012343; Glyco_trans_sub.
DR   Pfam; PF00686; CBM_20; 1.
DR   Pfam; PF00723; Glyco_hydro_15; 1.
DR   PIRSF; PIRSF001031; Glu-a-glcsd_SBD; 1.
```